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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/048,116

DATE: 07/17/2002
TIME: 09:33:37

Input Set : A:\EP.txt
Output Set: N:\CRF3\07172002\J048116.raw

3 <110> APPLICANT: C.N.R.S.
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED FROM
 THESE PROTEINS,
 6 ANALOGOUS TO MOLECULES INVOLVED IN IMMUNE RESPONSES
 8 <130> FILE REFERENCE: CP/BB 1181
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/048,116
 C--> 11 <141> CURRENT FILING DATE: 2002-05-24
 13 <160> NUMBER OF SEQ ID NOS: 2
 15 <170> SOFTWARE: PatentIn Ver. 2.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1484
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial sequence
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(1482)
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Description of Artificial Sequence: ligation
 28 fragments of DNA
 30 <400> SEQUENCE: 1
 31 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc 48
 32 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
 33 1 5 10 15
 35 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta. 96
 36 Met Leu Ser Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
 37 20 25 30
 39 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag 144
 40 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
 41 35 40 45
 43 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat 192
 44 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
 45 50 55 60
 47 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc 240
 48 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
 49 65 70 75 80
 51 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac 288
 52 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
 53 85 90 95
 55 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag 336
 56 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
 57 100 105 110
 59 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag 384
 60 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
 61 115 120 125

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63	ccc	aac	acc	ctt	atc	tgc	ttt	gtg	gac	aac	atc	ttc	cca	cct	gtg	atc	432
64	Pro	Asn	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile	
65	130					135					140						
67	aac	atc	aca	tgg	ctc	aga	aat	agc	aag	tca	gtc	aca	gac	ggc	gtt	tat	480
68	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr	
69	145					150					155					160	
71	gag	acc	agc	ttc	ctc	gtc	aac	cgt	gac	cat	tcc	ttc	cac	aag	ctg	tct	528
72	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser	
73						165				170					175		
75	tat	ctc	acc	ttc	atc	cct	tct	gat	gat	gac	att	tat	gac	tgc	aag	gtg	576
76	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	
77						180				185					190		
79	gag	cac	tgg	ggc	ctg	gag	gag	ccg	gtt	ctg	aaa	cac	tgg	gaa	cct	gag	624
80	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	
81						195			200			205					
83	att	cca	gcc	ccc	atg	tca	gag	ctg	aca	gaa	act	gga	ggt	gga	gga	tcc	672
84	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Gly	Ser	
85						210			215			220					
87	act	aca	gct	cca	tca	gct	cag	ctc	gaa	aaa	gag	ctc	cag	gcc	ctg	gag	720
88	Thr	Thr	Ala	Pro	Ser	Ala	Gln	Leu	Glu	Lys	Glu	Leu	Gln	Ala	Leu	Glu	
89	225					230				235					240		
91	aag	gaa	aat	gca	cag	ctg	gaa	tgg	gag	ttg	caa	gca	ctg	gaa	aag	gaa	768
92	Lys	Glu	Asn	Ala	Gln	Leu	Glu	Trp	Glu	Leu	Gln	Ala	Leu	Glu	Lys	Glu	
93						245				250			255				
95	ctg	gct	cag	gca	gca	tct	gag	ccc	aga	ggg	ccc	aca	atc	aag	ccc	tgt	816
96	Leu	Ala	Gln	Ala	Ala	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	
97						260			265			270					
99	cct	cca	tgc	aaa	tgc	cca	gca	cct	aac	ctc	ttg	ggt	gga	cca	tcc	gtc	864
100	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	
101						275			280			285					
103	ttc	atc	ttc	cct	cca	aag	atc	aag	gat	gta	ctc	atg	atc	tcc	ctg	agc	912
104	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	
105						290			295			300					
107	ccc	ata	gtc	aca	tgt	gtg	gtg	gtg	gat	gtc	agg	gat	gac	cca	gat		960
108	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	
109	305					310				315			320				
111	gtc	cag	atc	agc	tgg	ttt	gtg	aac	aac	gtg	gaa	gta	cac	aca	gct	cag	1008
112	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr	Ala	Gln	
113						325				330			335				
115	aca	caa	acc	cat	aga	gag	gat	tac	aac	agt	act	ctc	cg	gtg	gtc	agt	1056
116	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val	Val	Ser	
117						340			345			350					
119	gcc	ctc	ccc	atc	cag	cac	cag	gac	tgg	atg	agt	ggc	aag	gag	ttc	aaa	1104
120	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	
121						355			360			365					
123	tgc	aag	gtc	aac	aac	aaa	gac	ctc	cca	gct	ccc	atc	gag	aga	acc	atc	1152
124	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	
125						370			375			380					
127	tca	aaa	ccc	aaa	ggg	tca	gt	aga	gct	cca	cag	gt	ta	t	gtc	ttg	1200

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128 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro			
129 385 390 395 400			
131 cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc tgc atg	1248		
132 Pro Pro Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met			
133 405 410 415			
135 gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc aac aac	1296		
136 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn			
137 420 425 430			
139 ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg gac tct	1344		
140 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser			
141 435 440 445			
143 gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag aag aac	1392		
144 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn			
145 450 455 460			
147 tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg	1440		
148 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu			
149 465 470 475 480			
151 cac aat cac cac acg act aag agc ttc tcc cggtt act ccg ggt aa	1484		
152 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly			
153 485 490			
157 <210> SEQ ID NO: 2			
158 <211> LENGTH: 921			
159 <212> TYPE: DNA			
160 <213> ORGANISM: Artificial sequence			
162 <220> FEATURE:			
163 <223> OTHER INFORMATION: Description of artificial sequence: Ligation			
164 fragments of DNA			
166 <220> FEATURE:			
167 <221> NAME/KEY: CDS			
168 <222> LOCATION: (1)..(921)			
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172 Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val			
173 1 5 10 15			
175 ctg atg gtg ctg agc agc ccc ggg act gag ggc gga aac tcc atc tgc	96		
176 Leu Met Val Leu Ser Ser Pro Gly Thr Glu Gly Gly Asn Ser Ile Cys			
177 20 25 30			
179 ttc tcg ccg tcg ctg gag cac ccg atc gtg gtg tcc ggc agc tgg gac	144		
180 Phe Ser Pro Ser Leu Glu His Pro Ile Val Val Ser Gly Ser Trp Asp			
181 35 40 45			
183 gga ggt ggg ggc tca cta gtg ccc cga ggc tct gga ggt gga ggc tcc	192		
184 Gly Gly Gly Ser Leu Val Pro Arg Gly Ser Gly Gly Gly Ser			
185 50 55 60			
187 gaa agg cat ttc gtg gtc cag ttc aag ggc gag tgc tac tac acc aac	240		
188 Glu Arg His Phe Val Val Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn			
189 65 70 75 80			
191 ggg acg cag cgc ata cgg ctc gtg acc aga tac atc tac aac cgg gag	288		
192 Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu			
193 85 90 95			

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195	gag tac gtg cgc tac gac agc gac gtg ggc gag tac cgc gcg gtg acc	336
196	Glu Tyr Val Arg Tyr Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr	
197	100 105 110	
199	gag ctg ggg cgg cca gac gcc gag tac tgg aac agc cag ccg gag atc	384
200	Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile	
201	115 120 125	
203	ctg gag cga acg cgg gcc gag gtg gac acg gcg tgc aga cac aac tac	432
204	Leu Glu Arg Thr Arg Ala Glu Val Asp Thr Ala Cys Arg His Asn Tyr	
205	130 135 140	
207	gag ggg ccg gag acc agc acc tcc ctg cgg cgg ctt gaa cag ccc aat	480
208	Glu Gly Pro Glu Thr Ser Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn	
209	145 150 155 160	
211	gtc gcc atc tcc ctg tcc agg aca gag gcc ctc aac cac cac aac act	528
212	Val Ala Ile Ser Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr	
213	165 170 175	
215	ctg gtc tgt tcg gtg aca gat ttc tac cca gcc aag atc aaa gtg cgc	576
216	Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg	
217	180 185 190	
219	tgg ttc agg aat ggc cag gag aca gtg ggg gtc tca tcc aca cag	624
220	Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln	
221	195 200 205	
223	ctt att agg aat ggg gac tgg acc ttc cag gtc gtc atg ctg gag	672
224	Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu	
225	210 215 220	
227	atg acc cct cat cag gga gag gtc tac acc tgc cat gtg gag cat ccc	720
228	Met Thr Pro His Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro	
229	225 230 235 240	
231	agc ctg aag agc ccc atc act gtg gag tgg agg gca cag tcc gag tct	768
232	Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser	
233	245 250 255	
235	gcc cgg agc aag gga ggt gga gga tcc act aca gct cca tca gct cag	816
236	Ala Arg Ser Lys Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln	
237	260 265 270	
239	tgg aaa aag aaa ttg caa gca ctg aag aaa aag aac gct cag ctg aag	864
240	Leu Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys	
241	275 280 285	
243	tgg aaa ctt caa gcc ctc aag aag aaa ctc gcc cag cat cat cat cat	912
244	Trp Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln His His His His	
245	290 295 300	
247	cat cat tga	921
248	His His	
249	305	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/17/2002
PATENT APPLICATION: US/10/048,116 TIME: 09:33:38

Input Set : A:\EP.txt
Output Set: N:\CRF3\07172002\J048116.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY
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DATE: 07/17/2002
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Input Set : A:\EP.txt
Output Set: N:\CRF3\07172002\J048116.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date